



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,495

DATE: 06/04/2002

TIME: 14:51:10

Input Set : A:\pf0698usn.txt

Output Set: N:\CRF3\06042002\J019495.raw

P.6

ENTERED

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1 <110> APPLICANT: Hillman, Jennifer L.
2   Bandman, Olga
3   Tang, Y. Tom
4   Lal, Preeti
5   Yue, Henry
6   Reddy, Roopa
7   Azimzai, Yalda
8   Baughn, Mariah R.
10 <120> TITLE OF INVENTION: HUMAN MEMBRANE-ASSOCIATED PROTEINS
12 <130> FILE REFERENCE: PF-0698 PCT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/019,495
C--> 15 <141> CURRENT FILING DATE: 2002-04-15
17 <160> NUMBER OF SEQ ID NOS: 34
19 <170> SOFTWARE: PERL Program
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 175
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <223> OTHER INFORMATION: 402771CD1
31 <400> SEQUENCE: 1
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33   1           5           10           15
34 Ser Ala Leu Gly Pro Gly Ala Gly Ala Ala Gln Pro Ser Ala Ser
35           20           25           30
36 Pro Leu Glu Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala
37           35           40           45
38 Ala Leu Leu Lys Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe
39           50           55           60
40 Ile Cys Val Arg Ser Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser
41           65           70           75
42 Tyr Phe Glu Val Val Thr Ile Cys Asp Leu Ile Met Ile Leu Ala
43           80           85           90
44 Phe Tyr Leu Val His Leu Phe Arg Phe Tyr Arg Val Leu Thr Cys
45           95          100          105
46 Ile Ser Trp Pro Leu Ser Glu Leu Leu His Tyr Leu Ile Gly Thr
47          110          115          120
48 Leu Leu Leu Leu Ile Ala Ser Ile Val Ala Ala Ser Lys Ser Tyr
49          125          130          135
50 Asn Gln Ser Gly Leu Val Ala Gly Ala Ile Phe Gly Phe Met Ala
51          140          145          150
52 Thr Phe Leu Cys Met Ala Ser Ile Trp Leu Ser Tyr Lys Ile Ser
53          155          160          165

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54 Cys Val Thr Gln Ser Thr Asp Ala Ala Val
55           170           175
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 161
60 <212> TYPE: PRT
61 <213> ORGANISM: Homo sapiens
63 <220> FEATURE:
64 <223> OTHER INFORMATION: 1296216CD1
66 <400> SEQUENCE: 2
67 Met Leu Asn Trp Ile Ile Arg Leu Gln Ala Ile Leu Glu Ile Ile
68 1           5           10           15
69 Thr Ser Glu Thr Gly Arg Ala Leu Thr Leu Leu Ala Gln Gln Glu
70           20           25           30
71 Thr Gln Met Arg Asn Ala Ile Tyr Gln Asn Arg Leu Ala Leu Asp
72           35           40           45
73 Tyr Leu Leu Ala Ala Glu Gly Gly Val Cys Glu Lys Phe Asn Leu
74           50           55           60
75 Thr Lys Cys Cys Leu Gln Arg Asp Asp Gln Gly Gln Val Val Lys
76           65           70           75
77 Asn Ile Val Arg Asp Met Thr Lys Leu Ala His Val Pro Met Gln
78           80           85           90
79 Val Trp His Arg Phe Asp Pro Gly Ser Leu Phe Gly Lys Trp Leu
80           95          100          105
81 Pro Ala Leu Gly Gly Phe Lys Thr Leu Ile Ile Gly Met Ile Met
82          110          115          120
83 Val Leu Gly Thr Cys Met Leu Leu Pro Cys Met Leu Pro Ile Phe
84          125          130          135
85 Leu Gln Leu Leu Arg Ser Phe Val Ile Thr Leu Val His Gln Lys
86          140          145          150
87 Thr Ser Ala Gln Val Tyr Tyr Met Asn His Tyr
88          155          160
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 563
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <220> FEATURE:
97 <223> OTHER INFORMATION: 1693173CD1
99 <400> SEQUENCE: 3
100 Met Pro Asn Gly Ser Thr Ile Pro Pro Gly Ser Pro Glu Glu Met
101 1           5           10           15
102 Leu Phe His Phe Gly Met Thr Trp Gln Ile Asn Gly Thr Gly Leu
103           20           25           30
104 Leu Gly Lys Arg Asn Asp Gln Leu Pro Ser Asn Phe Thr Pro Val
105           35           40           45
106 Phe Tyr Ser Gln Leu Gln Lys Asn Ser Ser Trp Ala Glu His Leu
107           50           55           60
108 Ile Ser Asn Cys Asp Gly Asp Ser Ser Cys Ile Tyr Asp Thr Leu
109           65           70           75
110 Ala Leu Arg Asn Ala Ser Ile Gly Leu His Thr Arg Glu Val Ser

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111		80		85		90
112	Lys Asn Tyr Glu Gln Ala Asn Ala Thr		Leu Asn Gln Tyr Pro Pro			
113		95		100		105
114	Ser Ile Asn Gly Gly Arg Val Ile Glu		Ala Tyr Lys Gly Gln Thr			
115		110		115		120
116	Thr Leu Ile Gln Tyr Thr Ser Asn Ala		Glu Asp Ala Asn Phe Thr			
117		125		130		135
118	Leu Arg Asp Ser Cys Thr Asp Leu Glu		Leu Phe Glu Asn Gly Thr			
119		140		145		150
120	Leu Leu Trp Thr Pro Lys Ser Leu Glu		Pro Phe Thr Leu Glu Ile			
121		155		160		165
122	Leu Ala Arg Ser Ala Lys Ile Gly Leu		Ala Ser Ala Leu Gln Pro			
123		170		175		180
124	Arg Thr Val Val Cys His Cys Asn Ala		Glu Ser Gln Cys Leu Tyr			
125		185		190		195
126	Asn Gln Thr Ser Arg Val Gly Asn Ser		Ser Leu Glu Val Ala Gly			
127		200		205		210
128	Cys Lys Cys Asp Gly Gly Thr Phe Gly		Arg Tyr Cys Glu Gly Ser			
129		215		220		225
130	Glu Asp Ala Cys Glu Glu Pro Cys Phe		Pro Ser Val His Cys Val			
131		230		235		240
132	Pro Gly Lys Gly Cys Glu Ala Cys Pro		Pro Asn Leu Thr Gly Asp			
133		245		250		255
134	Gly Arg His Cys Ala Ala Leu Gly Ser		Ser Phe Leu Cys Gln Asn			
135		260		265		270
136	Gln Ser Cys Pro Val Asn Tyr Cys Tyr		Asn Gln Gly His Cys Tyr			
137		275		280		285
138	Ile Ser Gln Thr Leu Gly Cys Gln Pro		Met Cys Thr Cys Pro Pro			
139		290		295		300
140	Ala Phe Thr Asp Ser Arg Cys Phe Leu		Ala Gly Asn Asn Phe Ser			
141		305		310		315
142	Pro Thr Val Asn Leu Glu Leu Pro Leu		Arg Val Ile Gln Leu Leu			
143		320		325		330
144	Leu Ser Glu Glu Glu Asn Ala Ser Met		Ala Glu Val Asn Ala Ser			
145		335		340		345
146	Val Ala Tyr Arg Leu Gly Thr Leu Asp		Met Arg Ala Phe Leu Arg			
147		350		355		360
148	Asn Ser Gln Val Glu Arg Ile Asp Ser		Ala Ala Pro Ala Ser Gly			
149		365		370		375
150	Ser Pro Ile Gln His Trp Met Val Ile		Ser Glu Phe Gln Tyr Arg			
151		380		385		390
152	Pro Arg Gly Pro Val Ile Asp Phe Leu		Asn Asn Gln Leu Leu Ala			
153		395		400		405
154	Ala Val Val Glu Ala Phe Leu Tyr His		Val Pro Arg Arg Ser Glu			
155		410		415		420
156	Glu Pro Arg Asn Asp Val Val Phe Gln		Pro Ile Ser Gly Glu Asp			
157		425		430		435
158	Val Arg Asp Val Thr Ala Leu Asn Val		Ser Thr Leu Lys Ala Tyr			
159		440		445		450

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160 Phe Arg Cys Asp Gly Tyr Lys Gly Tyr Asp Leu Val Tyr Ser Pro
161                               455                               460                               465
162 Gln Ser Gly Phe Thr Cys Val Ser Pro Cys Ser Arg Gly Tyr Cys
163                               470                               475                               480
164 Asp His Gly Gly Gln Cys Gln His Leu Pro Ser Gly Pro Arg Cys
165                               485                               490                               495
166 Ser Cys Val Ser Phe Ser Ile Tyr Thr Ala Trp Gly Glu His Cys
167                               500                               505                               510
168 Glu His Leu Ser Met Lys Leu Asp Ala Phe Phe Gly Ile Phe Phe
169                               515                               520                               525
170 Gly Val Leu Gly Gly Leu Leu Leu Leu Gly Val Gly Thr Phe Val
171                               530                               535                               540
172 Val Leu Arg Phe Trp Gly Cys Ser Gly Ala Arg Phe Ser Tyr Phe
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174 Leu Asn Ser Ala Glu Ala Leu Pro
175                               560
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 396
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <220> FEATURE:
184 <223> OTHER INFORMATION: 2095069CD1
186 <400> SEQUENCE: 4
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188 1 5 10 15
189 Val Gln Glu Tyr Pro Thr Leu Lys Val Pro Tyr Glu Thr Leu Asn
190 20 25 30
191 Lys Arg Phe Arg Ala Ala Gln Lys Asn Ile Asp Arg Glu Thr Ser
192 35 40 45
193 His Val Thr Met Val Val Ala Glu Leu Glu Lys Thr Leu Ser Gly
194 50 55 60
195 Cys Pro Ala Val Asp Ser Val Val Ser Leu Leu Asp Gly Val Val
196 65 70 75
197 Glu Lys Leu Ser Val Leu Lys Arg Lys Ala Val Glu Ser Ile Gln
198 80 85 90
199 Ala Glu Asp Glu Ser Ala Lys Leu Cys Lys Arg Arg Ile Glu His
200 95 100 105
201 Leu Lys Glu His Ser Ser Asp Gln Pro Ala Ala Ala Ser Val Trp
202 110 115 120
203 Lys Arg Lys Arg Met Asp Arg Met Met Val Glu His Leu Leu Arg
204 125 130 135
205 Cys Gly Tyr Tyr Asn Thr Ala Val Lys Leu Ala Arg Gln Ser Gly
206 140 145 150
207 Ile Glu Asp Leu Val Asn Ile Glu Met Phe Leu Thr Ala Lys Glu
208 155 160 165
209 Val Glu Glu Ser Leu Glu Arg Arg Glu Thr Ala Thr Cys Leu Ala
210 170 175 180
211 Trp Cys His Asp Asn Lys Ser Arg Leu Arg Lys Met Lys Ser Cys
212 185 190 195

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213	Leu	Glu	Phe	Ser	Leu	Arg	Ile	Gln	Glu	Phe	Ile	Glu	Leu	Ile	Arg
214					200					205					210
215	Gln	Asn	Lys	Arg	Leu	Asp	Ala	Val	Arg	His	Ala	Arg	Lys	His	Phe
216					215					220					225
217	Ser	Gln	Ala	Glu	Gly	Ser	Gln	Leu	Asp	Glu	Val	Arg	Gln	Ala	Met
218					230					235					240
219	Gly	Met	Leu	Ala	Phe	Pro	Pro	Asp	Thr	His	Ile	Ser	Pro	Tyr	Lys
220					245					250					255
221	Asp	Leu	Leu	Asp	Pro	Ala	Arg	Trp	Arg	Met	Leu	Ile	Gln	Gln	Phe
222					260					265					270
223	Arg	Tyr	Asp	Asn	Tyr	Arg	Leu	His	Gln	Leu	Gly	Asn	Asn	Ser	Val
224					275					280					285
225	Phe	Thr	Leu	Thr	Leu	Gln	Ala	Gly	Leu	Ser	Ala	Ile	Lys	Thr	Pro
226					290					295					300
227	Gln	Cys	Tyr	Lys	Glu	Asp	Gly	Ser	Ser	Lys	Ser	Pro	Asp	Cys	Pro
228					305					310					315
229	Val	Cys	Ser	Arg	Ser	Leu	Asn	Lys	Leu	Ala	Gln	Pro	Leu	Pro	Met
230					320					325					330
231	Ala	His	Cys	Ala	Asn	Ser	Arg	Leu	Val	Cys	Lys	Ile	Ser	Gly	Asp
232					335					340					345
233	Val	Met	Asn	Glu	Asn	Asn	Pro	Pro	Met	Met	Leu	Pro	Asn	Gly	Tyr
234					350					355					360
235	Val	Tyr	Gly	Tyr	Asn	Ser	Leu	Leu	Ser	Ile	Arg	Gln	Asp	Asp	Lys
236					365					370					375
237	Val	Val	Cys	Pro	Arg	Thr	Lys	Glu	Val	Phe	His	Phe	Ser	Gln	Ala
238					380					385					390
239	Glu	Lys	Val	Tyr	Ile	Met									
240					395										
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244	<211> LENGTH: 265														
245	<212> TYPE: PRT														
246	<213> ORGANISM: Homo sapiens														
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249	<223> OTHER INFORMATION: 2645927CD1														
251	<400> SEQUENCE: 5														
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253	1				5					10					15
254	Gln	Phe	Asn	Glu	Asn	Glu	Ala	Ile	Gln	Trp	Met	Gln	Glu	Asn	Trp
255					20					25					30
256	Lys	Lys	Ser	Phe	Leu	Phe	Ser	Ala	Leu	Tyr	Ala	Ala	Phe	Ile	Phe
257					35					40					45
258	Gly	Gly	Arg	His	Leu	Met	Asn	Lys	Arg	Ala	Lys	Phe	Glu	Leu	Arg
259					50					55					60
260	Lys	Pro	Leu	Val	Leu	Trp	Ser	Leu	Thr	Leu	Ala	Val	Phe	Ser	Ile
261					65					70					75
262	Phe	Gly	Ala	Leu	Arg	Thr	Gly	Ala	Tyr	Met	Val	Tyr	Ile	Leu	Met
263					80					85					90
264	Thr	Lys	Gly	Leu	Lys	Gln	Ser	Val	Cys	Asp	Gln	Gly	Phe	Tyr	Asn
265					95					100					105

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/019,495

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; N Pos. 3607